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Sequence Listing was accepted.

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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=8; day=28; hr=10; min=10; sec=1; ms=415; ]

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Application No: 10586111

Version No: 2.1

Input Set:

Output Set:

Started: 2008-08-28 10:05:09.924

Finished: 2008-08-28 10:05:12.068

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 144 ms

Total Warnings: 9

Total Errors: 0

No. of SeqIDs Defined: 9

Actual SeqID Count: 9

Error code	Error Description
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<110> Fraunhofer Gesellschaft zur Förderung der angewandten  
Forschung e.V.

<130> 3581.10-US-01

<141> 2006-07-14

<151> 2005-01-13

<151> 2004-01-16

<151> 2004-07-29

<160> 9

<170> PatentIn version 3.5

<211> 1785

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence: pMS-(L-DAPK2'-Ki-4)-III/G  
open reading frame (ORF)

 $\langle 220 \rangle$ 

<221> N\_region

 $\langle 222 \rangle \quad (1) \dots (21)$ 

<223> immunoglobulin kappa chain leader sequence

 $\langle 220 \rangle$ 

<221> CDS

<222> (1) . . (1785)

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15

ggt tcc act ggt gac tct aga atg gtc cag gcc tcg atg agg agc cca 96  
Gly Ser Thr Gly Asp Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro  
20 25 30

aat atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att 144  
Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile  
35 40 45

gga gag gag ctg ggc agt ggc cag ttt gcc atc gtg aag aag tgc cgg	192
Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg	
50 55 60	
 gag aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg	240
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg	
65 70 75 80	
 cag agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg	288
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg	
85 90 95	
 gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg	336
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu	
100 105 110	
 cac gac gtc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta	384
His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu	
115 120 125	
 gtg tcc gga gga gaa ctg ttt gat ttc ctg gcc cag aag gag tcg tta	432
Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu	
130 135 140	
 agt gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg	480
Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val	
145 150 155 160	
 aat tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa	528
Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu	
165 170 175	
 aac atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg	576
Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu	
180 185 190	
 att gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa	624
Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys	
195 200 205	
 aac att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat	672
Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr	
210 215 220	
 aac att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat	720
Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr	
225 230 235 240	
 tat atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa	768
Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln	
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 gaa acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa	816
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu	
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Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu	
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ctt gtg aaa gag acc cgg aaa cgg ctt acc atc caa gag gct ctc aga	912
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg	
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His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala	
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Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser Gly Tyr	
340 345 350	
acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct gga cag	1104
Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln	
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Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp	
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tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac aaa tcc	1200
Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser	
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Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser	
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gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg ggg ttt	1296
Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe	
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cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc	1344
Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly	
435 440 445	
ggg tca ggc gga ggt ggc tct ggc ggt ggc gga tgc gac att gtg ctg	1392
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu	
450 455 460	
acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg gtc acc	1440
Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr	
465 470 475 480	
ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc tgg tat	1488
Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr	
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caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg gcc tcc	1536
Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser	



Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg  
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Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu  
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His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu  
115 120 125

Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu  
130 135 140

Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val  
145 150 155 160

Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu  
165 170 175

Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu  
180 185 190

Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys  
195 200 205

Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr  
210 215 220

Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr  
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Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln  
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Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu  
260 265 270

Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu  
275 280 285

Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg  
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His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala

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Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp			
370	375	380	
Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser			
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Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser			
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Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly			
515	520	525	
Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala			
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Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala  
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 ggt tcc act ggt gac gcg gcc cag ccg gcc atg gcc cag gtc aag ctg 96  
 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu  
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 cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg 144  
 Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met  
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 tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg 192  
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 65 70 75 80

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Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala	
85 90 95	
aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc	336
Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg	
100 105 110	
agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca	384
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr	
115 120 125	
act cag act acg tgg ggg ttt cct ttt tgg ggc caa ggg acc acg gtc	432
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Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
145 150 155 160	
ggc gga tcg gac att gtg ctg acc cag tct cca aaa tcc atg gcc atg	528
Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met	
165 170 175	
tca gtc gga gag agg gtc acc ttg agc tgc aag gcc agt gag aat gtg	576
Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val	
180 185 190	
gat tct ttt gtt tcc tgg tat caa cag aaa cca ggc cag tct cct aaa	624
Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	